



# CDS: isp6



WARNING: 30th July 2008

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## General Information

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|                 |   |
|-----------------|---|
| Name            | isp6  |
| Systematic Name | SPAC4A8.04                                  |
| Gene Synonyms   | prb1  |
| Status          | experimentally characterised (or published) |
| Product         | vacuolar serine protease Isp6               |
| Type            | CDS   |
| Sequence        | <a href="#">DNA and Protein</a>             |

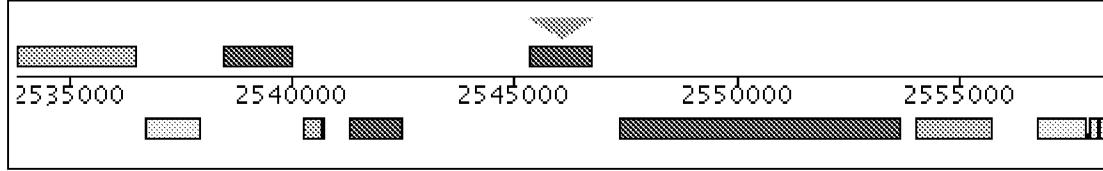
## Location

|                 |  |
|-----------------|--|
| Chromosome      | 1  |
| Contig Location | 2545350..2546753 (Unspliced length: 1404 bp) |
| Exons           | 2545350..2546753 (Spliced length: 1404 bp)   |

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## Context Map:



SPAC25H1.07 SPAC25H1.08c mde5 SPAC4A8.02c ptc4 >isp6< myp2 SPAC4A8.06c SPAC4A8.07c

## Curation

|   |                               |                                    |
|---|-------------------------------|------------------------------------|
| Term  | Db xref/URL                   | Other genes annotated to this term |
| expressed during nitrogen starvation                    | <a href="#">PMID:11872168</a> | (2 Others)                         |
| conserved eukaryotic family                             |                               | (866 Others)                       |
| similar to <i>S. cerevisiae</i> <a href="#">YEL060C</a> |                               | (1 Other)                          |
| similar to <i>S. pombe</i> <a href="#">SPAC1006.01</a>  |                               | (0 Others)                         |

## Predicted Peptide Properties

|                   |  |             |       |
|-------------------|--|-------------|-------|
| Mass              | 49.3 kDa   | Amino acids | 467   |
| Isoelectric point | pH 5.2   | Charge      | -12.0 |
| Signal Peptide    | Signal peptide predicted for SPAC4A8.04 by SignalP 2.0 HMM (Signal peptide probability 0.999, signal anchor probability 0.000) with cleavage site probability 0.874 between residues 24 and 25 |             |       |

|                       |  |
|-----------------------|--|
| Transmembrane Domains | 0 found  |
| GPI Anchor            | GPI-Anchor Signal predicted for SPAC4A8.04 by DGPI v2.04 with cleavage site probability 1.5480001 near 430 |

### Gene Ontology Annotation

| Term (browse Amigo)   | Qualifier Evidence                               | Other genes annotated to this term |
|---|--|------------------------------------|
| <b>Biological Process</b>   |  |                                    |
| <u>RNA catabolic process</u>                                      | IGI (PMID:11872168) with pnu1                    | <u>75 others</u>                   |
| <u>autophagy</u>  | IMP (PMID:16550352)                              | <u>24 others</u>                   |
| <u>cellular response to nitrogen starvation</u>                   | IEP (PMID:11872168)                              | <u>30 others</u>                   |
| <u>cellular response to nitrogen starvation</u>                   | IMP (PMID:16550352)                              | <u>30 others</u>                   |
| <u>conjugation with cellular fusion</u>                           | IMP (PMID:7954893)                               | <u>103 others</u>                  |
| <u>proteolysis involved in cellular protein catabolic process</u> | IMP (PMID:11872168)                              | <u>167 others</u>                  |
| <u>regulation of nitrogen compound metabolic process</u>          | IMP (PMID:16550352)                              | <u>5 others</u>                    |
| <u>vacuole organization and biogenesis</u>                        | IMP (PMID:16550352)                              | <u>44 others</u>                   |
| <b>Cellular Component</b>   |  |                                    |
| <u>Golgi apparatus</u>  | IDA (PMID:16823372)                              | <u>356 others</u>                  |
| <u>vacuole</u>  | TAS (PMID:16550352)                              | <u>145 others</u>                  |
| <b>Molecular Function</b>   |  |                                    |
| <u>serine-type endopeptidase activity</u>                         | IEA (GOA:spkw GO_REF:0000004) with SP_KW:KW-0720 | <u>13 others</u>                   |
| <u>serine-type peptidase activity</u>                             | ISS (PMID:17072883) with Pfam:PF00082            | <u>18 others</u>                   |

### Catalytic Activity

EC 3.4.21.- : [IUBMB](#)EC 3.4.24.- : [IUBMB](#)

### Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)TranscriptomeViewer [SPAC4A8.04](#) High-resolution view of transcripts in neighbourhood

### Literature

Search for [isp6](#) in PubMed

### Domain Information

[View Pfam domain structure for this gene product](#)[View SCOP superfamily](#)

| DB       | Accs                      | Description  |
|----------|---------------------------|--|
| Pfam     | <a href="#">PF05922</a>   | Subtilisin N-terminal Region                       |
| Pfam     | <a href="#">PF00082</a>   | Subtilase family                                   |
| MEROPS   | <a href="#">S08.052</a>   | MEROPS   |
| InterPro | <a href="#">IPR000209</a> | Peptidase S8 and S53, subtilisin, kexin, sedolisin |
| InterPro | <a href="#">IPR010259</a> | Proteinase inhibitor I9, subtilisin propeptide     |
| InterPro | <a href="#">IPR015500</a> | Subtilisin-related serine protease                 |

|         |                         |  |
|---------|-------------------------|--|
| PRINTS  | <a href="#">PR00723</a> | Subtilisin serine protease family (S8) signature               |
| PROSITE | <a href="#">PS00136</a> | Serine proteases, subtilase family, aspartic acid active site. |
| PROSITE | <a href="#">PS00137</a> | Serine proteases, subtilase family, histidine active site.     |
| PROSITE | <a href="#">PS00138</a> | Serine proteases, subtilase family, serine active site.        |

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#### Database Cross-References

| DB               | Accs                       | Description   |
|------------------|----------------------------|---|
| UniProtKB        | <a href="#">P40903</a>     | Sexual differentiation process putative subtilase-type proteinase isp6 (EC 3.4.21.-). |
| EMBL             | <a href="#">D14063</a>     | Schizosaccharomyces pombe mRNA for serine protease, complete cds.                     |
| EMBL             | <a href="#">CU329670</a>   | Schizosaccharomyces pombe chromosome I  |
| Biotwiki         | <a href="#">SPAC4A8_04</a> | Biotwiki  |
| NCBI Entrez Gene | <a href="#">SPAC4A8.04</a> | NCBI Entrez Gene  |
| FYSSION          | <a href="#">SPAC4A8.04</a> | FYSSION   |
| GermOnline       | <a href="#">SPAC4A8.04</a> | GermOnline  |
| NBRP             | <a href="#">SPAC4A8.04</a> | Fission yeast strain database, National BioResource Project (Japan)                   |
| PIR              | <a href="#">S45493</a>     | PIR   |
| YOGY             | <a href="#">SPAC4A8.04</a> | Retrieval of eukaryotic orthologs   |

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#### UniProtKB Annotation For This Protein

|                     |  |
|---------------------|--|
| Developmental Stage | Transcribed specifically during sexual development.  |
| Similarity          | Belongs to the peptidase S8 family.  |
| Keywords            | Complete proteome (4982 others) , Hydrolase (451 others) , Protease (90 others) , Serine protease (8 others) |

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